

09/462625  
11 JAN 2000

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: Boehringer Ingelheim International GmbH  
(B) STREET: Binger Strasse 173  
(C) CITY: Ingelheim am Rhein  
(E) COUNTRY: Germany  
(F) POSTAL CODE (ZIP): 55216  
(G) TELEPHONE: 06132/772282  
(H) TELEFAX: 06132/774377

(ii) TITLE OF INVENTION: Tumor Growth Inhibition- and  
Apoptosis-Associated Genes and Polypeptides and  
Methods of Use Thereof

(iii) NUMBER OF SEQUENCES: 24

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (v) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 893 764  
(B) FILING DATE: 11-JUL-1997

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 549 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..549

0946262 : 078000

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Phe Ala Cys Ala Leu Leu Ala Leu Leu Gly Leu Ala Thr Ser  
1 5 10 15

Cys Ser Phe Ile Val Pro Arg Ser Glu Trp Arg Ala Leu Pro Ser Glu  
20 25 30

Cys Ser Ser Arg Leu Gly His Pro Val Arg Tyr Val Val Ile Ser His  
35 40 45

Thr Ala Gly Ser Phe Cys Asn Ser Pro Asp Ser Cys Glu Gln Gln Ala  
50 55 60

Arg Asn Val Gln His Tyr His Lys Asn Glu Leu Gly Trp Cys Asp Val  
65 70 75 80

Ala Tyr Asn Phe Leu Ile Gly Glu Asp Gly His Val Tyr Glu Gly Arg  
85 90 95

Gly Trp Asn Ile Lys Gly Asp His Thr Gly Pro Ile Trp Asn Pro Met  
100 105 110

Ser Ile Gly Ile Thr Phe Met Gly Asn Phe Met Asp Arg Val Pro Ala  
115 120 125

Lys Arg Ala Leu Arg Ala Ala Leu Asn Leu Leu Glu Cys Gly Val Ser  
130 135 140

Arg	Gly	Phe	Leu	Arg	Ser	Asn	Tyr	Glu	Val	Lys	Gly	His	Arg	Asp	Val
145					150					155					160

Gln Ser Thr Leu Ser Pro Gly Asp Gln Leu Tyr Gln Val Ile Gln Ser  
165 170 175

Trp Glu His Tyr Arg Glu  
180

**09-06-2017**

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens  
 (F) TISSUE TYPE: Bone Marrow

## (ix) FEATURE:

- (A) NAME/KEY: 5'UTR  
 (B) LOCATION:1..67

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION:68..643

## (ix) FEATURE:

- (A) NAME/KEY: 3'UTR  
 (B) LOCATION:644..718

## (ix) FEATURE:

- (A) NAME/KEY: polyA\_site  
 (B) LOCATION:712..714

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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CTGAGTTACT GGGCCCAGAG GCTGGGCCCC TGGACATGTA CCTGCAGCCA CTATGTCCCG      60
40 CCGCTCT ATG CTG CTT GCC TGG GCT CTC CCC AGC CTC CTT CGA CTC GGA      109
    Met Leu Leu Ala Trp Ala Leu Pro Ser Leu Leu Arg Leu Gly
      1              5              10

GCG GCT CAG GAG ACA GAA GAC CCG GCC TGC TGC AGC CCC ATA GTG CCC      157
45 Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys Ser Pro Ile Val Pro
   15              20              25              30

CGG AAC GAG TGG AAG GCC CTG GCA TCA GAG TGC GCC CAG CAC CTG AGC      205
50 Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu Cys Ala Gln His Leu Ser
      35              40              45

CTG CCC TTA CGC TAT GTG GTG GTA TCG CAC ACG GCG GGC AGC AGC TGC      253
    Leu Pro Leu Arg Tyr Val Val Val Ser His Thr Ala Gly Ser Ser Cys
      50              55              60

AAC ACC CCC GCC TCG TGC CAG CAG CAG GCC CGG AAT GTG CAG CAC TAC      301
55 Asn Thr Pro Ala Ser Cys Gln Gln Gln Ala Arg Asn Val Gln His Tyr
      65              70              75

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008220" 52929460

5	CAC ATG AAG ACA CTG GGC TGG TGC GAC GTG GGC TAC AAC TTC CTG ATT His Met Lys Thr Leu Gly Trp Cys Asp Val Gly Tyr Asn Phe Leu Ile 80 85 90	349
10	GGA GAA GAC GGG CTC GTA TAC GAG GGC CGT GGC TGG AAC TTC ACG GGT Gly Glu Asp Gly Leu Val Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly 95 100 105 110	397
15	GCC CAC TCA GGT CAC TTA TGG AAC CCC ATG TCC ATT GGC ATC AGC TTC Ala His Ser Gly His Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe 115 120 125	445
20	ATG GGC AAC TAC ATG GAT CGG GTG CCC ACA CCC CAG GCC ATC CGG GCA Met Gly Asn Tyr Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala 130 135 140	493
25	GCC CAG GGT CTA CTG GCC TGC GGT GTG GCT CAG GGA GCC CTG AGG TCC Ala Gln Gly Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser 145 150 155	541
30	AAC TAT GTG CTC AAA GGA CAC CGG GAT GTG CAG CGT ACA CTC TCT CCA Asn Tyr Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro 160 165 170	589
35	GGC AAC CAG CTC TAC CAC CTC ATC CAG AAT TGG CCA CAC TAC CGC TCC Gly Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser 175 180 185 190	637
40	CCC TGA GGCCCTGCTG ATCCGCACCC CATTCCTCCC CTCCCATGGC CAAAAACCCC Pro *	693
45	ACTGTCTCCT TCTCCAATAA AGATG	718

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Leu Leu Ala Trp Ala Leu Pro Ser Leu Leu Arg Leu Gly Ala Ala  
1 5 10 15

Gln Glu Thr Glu Asp Pro Ala Cys Cys Ser Pro Ile Val Pro Arg Asn  
20 25 30

Glu Trp Lys Ala Leu Ala Ser Glu Cys Ala Gln His Leu Ser Leu Pro  
35 40 45

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Leu Arg Tyr Val Val Val Ser His Thr Ala Gly Ser Ser Cys Asn Thr  
 50 55 60  
 5 Pro Ala Ser Cys Gln Gln Gln Ala Arg Asn Val Gln His Tyr His Met  
 65 70 75 80  
 Lys Thr Leu Gly Trp Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu  
 85 90 95  
 10 Asp Gly Leu Val Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His  
 100 105 110  
 Ser Gly His Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly  
 115 120 125  
 Asn Tyr Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln  
 130 135 140  
 20 Gly Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr  
 145 150 155 160  
 Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly Asn  
 165 170 175  
 25 Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser Pro \*  
 180 185 190

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: synthetic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT TTAC

14

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: synthetic DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATCGGGCTG

10

10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

25 AGTCAGCCAC

10

30 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAAAGGGCCT CGTGATAC

18

45

(2) INFORMATION FOR SEQ ID NO:9:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGGGCCCTC CACTCACTTG CATAGGCATT TGTAGC

36

10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

25 GCTACAAATG CCTATGCAAG TGAGTGGAGG GCCCTG

36

25

(2) INFORMATION FOR SEQ ID NO:11:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCGCTAGC CTGCAGTTAT CACTCTCGGT AGTGTTCCCA G

41

45

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCGGATCCG AGTGGAGGGC CCTGCCATCC

30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCGAATTCT TATCACTCTC GGTAGTGTTT

30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCCAGATCT CGTCCAGCAT GTTGTGTTGCC TGTGCT

36

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCACCAAAA TCAACGGGAC

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAGGGCCCTC CACTCACATC GTGCACCTGG G

31

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCAGGTGCA CGATGTGAGT GGAGGGCCCT G

31

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCCGCTAGC CTGCAGTTAT CACTCTCGGT AGTGTTCCCA G

41

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCCAAGCTT CCACCATGTC CCGCCGCTCT ATGCTG

36

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGAATTC TTATCAGGGG GAGCGGTAGT GTGG

34

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

5 Arg Ser Glu Trp Arg Ala Leu Pro Ser Glu Cys Ser Ser Arg Leu Gly  
1 5 10 15  
His Pro Tyr

10

## (2) INFORMATION FOR SEQ ID NO:22:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25 Gly Glu Asp Gly His Val Tyr Glu Gly Arg Gly Trp Asn Ile Lys Gly  
1 5 10 15  
30 Asp His Thr Gly Cys Tyr  
20

## (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

45 Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys Ser Pro Ile Val Pro Arg  
1 5 10 15  
50 Asn Glu Trp Lys Ala Leu Ala Ser Glu Tyr  
20 25

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J)

## (2) INFORMATION FOR SEQ ID NO:24:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

15

Gly Glu Asp Gly Leu Val Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly  
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Cys Tyr

009220"52929450

SEQUENCE LISTING

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Ala Tyr Asn Phe Leu Ile Gly Glu Asp Gly His Val Tyr Glu Gly Arg  
85 90 95

ggc tgg aac atc aag ggt gac cac aca ggg ccc atc tgg aat ccc atg 336  
Gly Trp Asn Ile Lys Gly Asp His Thr Gly Pro Ile Trp Asn Pro Met 110  
100 105

tct att ggc atc acc ttc atg ggg aac ttc atg gac cgg gta ccc gca 384  
Ser Ile Gly Ile Thr Phe Met Gly Asn Phe Met Asp Arg Val Pro Ala 125  
115 120

aag cgg gcc ctc cgt gct gcc cta aat ctt ctg gaa tgt ggg gtg tct 432  
Lys Arg Ala Leu Arg Ala Ala Leu Asn Leu Leu Glu Cys Gly Val Ser 140  
130 135

cgg ggc ttc ctg aga tcc aac tat gaa gtc aaa gga cac cgg gat gtg 480  
Arg Gly Phe Leu Arg Ser Asn Tyr Glu Val Lys Gly His Arg Asp Val 160  
145 150 155

caa agc act ctc tct cca ggt gac caa ctc tat cag gtc atc caa agc 528  
Gln Ser Thr Leu Ser Pro Gly Asp Gln Leu Tyr Gln Val Ile Gln Ser 175  
165 170

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Trp Glu His Tyr Arg Glu 180

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<212> PRT

<213> Artificial Sequence

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20 25 30  
Cys Ser Ser Arg Leu Gly His Pro Val Arg Tyr Val Val Ile Ser His  
35 40 45  
Thr Ala Gly Ser Phe Cys Asn Ser Pro Asp Ser Cys Glu Gln Gln Ala  
50 55 60  
Arg Asn Val Gln His Tyr His Lys Asn Glu Leu Gly Trp Cys Asp Val  
65 70 75 80  
Ala Tyr Asn Phe Leu Ile Gly Glu Asp Gly His Val Tyr Glu Gly Arg  
85 90 95  
Gly Trp Asn Ile Lys Gly Asp His Thr Gly Pro Ile Trp Asn Pro Met  
100 105 110  
Ser Ile Gly Ile Thr Phe Met Gly Asn Phe Met Asp Arg Val Pro Ala  
115 120 125  
Lys Arg Ala Leu Arg Ala Ala Leu Asn Leu Leu Glu Cys Gly Val Ser  
130 135 140  
Arg Gly Phe Leu Arg Ser Asn Tyr Glu Val Lys Gly His Arg Asp Val  
145 150 155 160  
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165 170 175  
Trp Glu His Tyr Arg Glu 180

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<212> DNA

003270"52929460

<213> Homo sapiens

<220>

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<222> (712)..(714)

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ccgctct atg ctg ctt gcc tgg gct ctc ccc agc ctc ctt cga ctc gga 109  
Met Leu Leu Ala Trp Ala Leu Pro Ser Leu Leu Arg Leu Gly  
1 5 10

gcg gct cag gag aca gaa gac ccg gcc tgc tgc agc ccc ata gtg ccc 157  
Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys Ser Pro Ile Val Pro  
15 20 25 30

cgg aac gag tgg aag gcc ctg gca tca gag tgc gcc cag cac ctg agc 205  
Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu Cys Ala Gln His Leu Ser  
35 40 45

ctg ccc tta cgc tat gtg gtg gta tgc cac acg gcg ggc agc agc tgc 253  
Leu Pro Leu Arg Tyr Val Val Val Ser His Thr Ala Gly Ser Ser Cys  
50 55 60

aac acc ccc gcc tcg tgc cag cag cag gcc cgg aat gtg cag cac tac 301  
Asn Thr Pro Ala Ser Cys Gln Gln Gln Ala Arg Asn Val Gln His Tyr  
65 70 75

cac atg aag aca ctg ggc tgg tgc gac gtg ggc tac aac ttc ctg att 349  
His Met Lys Thr Leu Gly Trp Cys Asp Val Gly Tyr Asn Phe Leu Ile  
80 85 90

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Gly Glu Asp Gly Leu Val Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly  
95 100 105 110

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Ala His Ser Gly His Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe  
115 120 125

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Met Gly Asn Tyr Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala  
130 135 140

gcc cag ggt cta ctg gcc tgc ggt gtg gct cag gga gcc ctg agg tcc 541  
Ala Gln Gly Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser  
145 150 155

aac tat gtg ctc aaa gga cac cgg gat gtg cag cgt aca ctc tct cca 589

002220"52222460



Asn Tyr Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro  
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 Gly Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser  
 175 180 185 190  
 ccc tga ggcctgctg atccgcaccc cattctctccc ctcccatggc caaaaacccc 693  
 Pro  
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 Glu Trp Lys Ala Leu Ala Ser Glu Cys Ala Gln His Leu Ser Leu Pro  
 35 40 45  
 Leu Arg Tyr Val Val Val Ser His Thr Ala Gly Ser Ser Cys Asn Thr  
 50 55 60  
 Pro Ala Ser Cys Gln Gln Gln Ala Arg Asn Val Gln His Tyr His Met  
 65 70 75 80  
 Lys Thr Leu Gly Trp Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu  
 85 90 95  
 Asp Gly Leu Val Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His  
 100 105 110  
 Ser Gly His Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly  
 115 120 125  
 Asn Tyr Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln  
 130 135 140  
 Gly Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr  
 145 150 155 160  
 Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly Asn  
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 Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser Pro  
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<220>  
 <223> Description of Artificial Sequence: DNA Primer

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14

<210> 6  
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008220-52929460

<220>  
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<212> DNA  
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<210> 8  
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<212> DNA  
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<210> 9  
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<210> 10  
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09462625-072800

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<220>  
<223> Description of Artificial Sequence: DNA Primer

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<210> 15  
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<223> Description of Artificial Sequence: DNA Primer

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<210> 16  
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<220>  
<223> Description of Artificial Sequence: DNA Primer

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008240 52929460

<210> 17  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: DNA Primer

<400> 17  
 cccaggtgca cgatgtgagt ggagggccct g 31

<210> 18  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: DNA Primer

<400> 18  
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<210> 19  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: DNA Primer

<400> 19  
 ggccaagctt ccaccatgtc ccgccgctct atgctg 36

<210> 20  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: DNA Primer

<400> 20  
 ggccgaattc ttatcagggg gagcggtagt gtgg 34

<210> 21  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: mutag7 peptide

<400> 21  
 Arg Ser Glu Trp Arg Ala Leu Pro Ser Glu Cys Ser Ser Arg Leu Gly  
 1 5 10 15

His Pro Tyr

008220"52929460

<220>  
<223> Description of Artificial Sequence: mutag7 peptide

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<210> 23
<211> 26
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: hutag7 peptide

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<210> 24
<211> 18
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: hutag7 peptide

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<400> 24
Gly Glu Asp Gly Leu Val Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly
  1             5             10             15
Cys Tyr
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